

Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) **EP 1 512 744 A1**

(12)

EUROPEAN PATENT APPLICATION

published in accordance with Art. 158(3) EPC

(43) Date of publication:
09.03.2005 Bulletin 2005/10

(51) Int Cl.7: **C12N 15/12, C12N 1/21,**
C12N 5/10, C07K 14/435,
C07K 19/00, G01N 21/78

(21) Application number: **03733346.5**

(22) Date of filing: **10.06.2003**

(86) International application number:
PCT/JP2003/007336

(87) International publication number:
WO 2003/104460 (18.12.2003 Gazette 2003/51)

(84) Designated Contracting States:
AT BE BG CH CY CZ DE DK EE ES FI FR GB GR
HU IE IT LI LU MC NL PT RO SE SI SK TR
Designated Extension States:
AL LT LV MK

(72) Inventors:
• **MIYAWAKI, Atsushi**
Wako-shi, Saitama 351-0198 (JP)
• **KARASAWA, Satoshi,**
Medical & Biol. Labs.Co.,Ltd.
Ina-shi, Nagano 396-0002 (JP)

(30) Priority: **10.06.2002 JP 2002168583**

(71) Applicants:
• **Riken**
Wako-shi, Saitama 351-0198 (JP)
• **Medical & Biological Laboratories Co., Ltd.**
Nagayo-shi, Aichi 460-0002 (JP)

(74) Representative:
Sternagel, Fleischer, Godemeyer & Partner
Patentanwälte,
An den Gärten 7
51491 Overath (DE)

(54) **PIGMENT PROTEIN**

(57) An object of the present invention is to provide a novel chromoprotein derived from *Cnidopus japonicus*. The present invention provides a chromoprotein derived from *Cnidopus japonicus* having the following properties:

(1) the absorption maximum wavelength is 610 nm, and fluorescence is not emitted;

(2) the molar absorption coefficient is 66,700 at 610 nm; and

(3) the pH sensitivity of light-absorbing property is stable at between pH 4 and pH 10.

EP 1 512 744 A1

Description

TECHNICAL FIELD

5 [0001] The present invention relates to a novel chromoprotein. More specifically, the present invention relates to a novel chromoprotein derived from *Cnidopus japonicus*, and the use thereof.

BACKGROUND ART

10 [0002] Green fluorescent protein (GFP) derived from *Aequorea victoria*, a jellyfish, has many purposes in biological systems. Recently, various GFP mutants have been produced based on the random mutagenesis and semi-rational mutagenesis, wherein a color is changed, a folding property is improved, luminance is enhanced, or pH sensitivity is modified. Fluorescent proteins such as GFP are fused with other proteins by gene recombinant technique, and monitoring of the expression and transportation of the fusion proteins is carried out.

15 [0003] One of the most commonly used types of GFP mutant is Yellow fluorescent protein (YFP). Among *Aequorea*-derived GFP mutants, YFP exhibits the fluorescence with the longest wavelength. The values ϵ and Φ of the majority of YFPs are 60,000 to 100,000 M⁻¹cm⁻¹ and 0.6 to 0.8, respectively (Tsien, R. Y. (1998). Ann. Rev. Biochem. 67, 509-544). These values are comparable to those of the general fluorescent group (fluorescein, rhodamine, etc.). Accordingly, improvement of the absolute luminance of YFP is nearly approaching its limit.

20 [0004] In addition, cyan fluorescent protein (CFP) is another example of the GFP mutant. Of this type of protein, ECFP (enhanced cyan fluorescent protein) has been known. Moreover, red fluorescent protein (RFP) has been isolated from sea anemone (*Discosoma sp.*). Of this type of protein, DasRed has been known. Thus, 4 types of fluorescent proteins, that are, green fluorescent protein, yellow fluorescent protein, cyan fluorescent protein, and red fluorescent protein, have successively been developed. The range of the spectrum has significantly been expanded.

DISCLOSURE OF THE INVENTION

[0005] An object of the present invention is to provide a novel chromoprotein derived from *Cnidopus japonicus*.

30 [0006] The present inventors have conducted intensive studies directed towards achieving the aforementioned object. They have designed suitable primers based on information regarding the amino acid sequences of known fluorescent proteins. Using these primers, they have succeeded in the amplification and cloning of a gene encoding a novel chromoprotein from the cDNA library of *Cnidopus japonicus* exhibiting a green color. The present inventors have further analyzed the light-absorbing properties and pH sensitivity of the obtained chromoprotein derived from *Cnidopus japonicus*. The present invention has been completed based on these findings.

35 [0007] That is to say, the present invention provides a chromoprotein derived from *Cnidopus japonicus* having the following properties:

- (1) the absorption maximum wavelength is 610 nm, and fluorescence is not emitted;
- (2) the molar absorption coefficient is 66,700 at 610 nm; and
- 40 (3) the pH sensitivity of light-absorbing property is stable at between pH 4 and pH 10.

[0008] In another aspect, the present invention provides a chromoprotein having either one of the following amino acid sequences:

- 45 (a) the amino acid sequence shown in SEQ ID NO: 1; and
- (b) an amino acid sequence comprising a deletion, substitution and/or addition of one or several amino acids with respect to the amino acid sequence shown in SEQ ID NO: 1, and having light-absorbing properties.

50 [0009] In another aspect, the present invention provides a chromoprotein capable of emitting fluorescence, which has an amino acid sequence, wherein, with respect to the amino acid sequence shown in SEQ ID NO: 1, alanine as an amino acid residue at position 28 is substituted by glycine, glutamic acid as an amino acid residue at position 41 is substituted by methionine, cysteine as an amino acid residue at position 145 is substituted by serine, and threonine as an amino acid residue at position 158 is substituted by isoleucine.

[0010] In another aspect, the present invention provides:

- 55 a chromoprotein having an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by leucine with respect to the amino acid sequence shown in SEQ ID NO: 1;
- a chromoprotein having an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is

substituted by methionine with respect to the amino acid sequence shown in SEQ ID NO: 1;

a chromoprotein having an amino acid sequence, wherein glutamic acid as an amino acid residue at position 41 is substituted by leucine, and phenylalanine as an amino acid residue at position 80 is substituted by glycine, with respect to the amino acid sequence shown in SEQ ID NO: 1;

a chromoprotein capable of emitting fluorescence, which has an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by phenylalanine with respect to the amino acid sequence shown in SEQ ID NO: 1;

a chromoprotein capable of emitting fluorescence, which has an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by histidine with respect to the amino acid sequence shown in SEQ ID NO: 1; and

a chromoprotein capable of emitting fluorescence, which has an amino acid sequence, wherein cysteine as an amino acid residue at position 26 is substituted by valine, cysteine as an amino acid residue at position 143 is substituted by serine, and proline as an amino acid residue at position 199 is substituted by leucine, with respect to the amino acid sequence shown in SEQ ID NO: 1.

[0011] In another aspect, the present invention provides DNA encoding the protein of the present invention.

[0012] In another aspect, the present invention provides either one of the following DNAs:

(a) DNA encoding the amino acid sequence shown in SEQ ID NO: 1; and

(b) DNA encoding an amino acid sequence, which comprises a deletion, substitution and/or addition of one or several amino acids with respect to the amino acid sequence shown in SEQ ID NO: 1, and has light-absorbing properties.

[0013] In another aspect, the present invention provides DNA having either one of the following nucleotide sequences:

(a) the nucleotide sequence shown in SEQ ID NO: 2; and

(b) a nucleotide sequence comprising a deletion, substitution and/or addition of one or several nucleotides with respect to the nucleotide sequence shown in SEQ ID NO: 2, and encoding a protein having light-absorbing properties.

[0014] In another aspect, the present invention provides DNA having the nucleotide sequence shown in any one of SEQ ID NOS: 12, 14, 16, 18, 20, or 22.

[0015] In another aspect, the present invention provides a recombinant vector having the DNA of the present invention.

[0016] In another aspect, the present invention provides a transformant having the DNA or recombinant vector of the present invention.

[0017] In another aspect, the present invention provides a fusion protein composed of the chromoprotein of the present invention and another protein.

[0018] In another aspect, the present invention provides a method for analyzing a physiologically active substance, which is characterized in that the FRET (fluorescence resonance energy transfer) method is applied using the chromoprotein of the present invention as an acceptor protein.

[0019] In another aspect, the present invention provides a light-absorbing reagent kit comprising the chromoprotein, DNA, recombinant vector, transformant, or fusion protein of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0020]

Figure 1 shows the results obtained by measuring the absorption spectrum of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention. The transverse axis indicates the wavelength of absorbed light, and the vertical axis indicates absorbance.

Figure 2 shows the pH sensitivity of the absorption spectrum of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention. The transverse axis indicates pH value, and the vertical axis indicates absorbance. 610 nm indicates the absorbance that is specific to the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention, and 277 nm indicates the absorbance (light absorption by aromatic amino acids) that is generally used as a quantitative amount of protein. In other words, it is shown that the amount of protein is constant at 277 nm, and the absorbance at 610 nm that is specific to the chromoprotein (KGr) derived from *Cnidopus*

japonicus of the present invention hardly changes in the range between pH 4 and pH 10.

Figure 3 shows the fluorescence spectrum of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting A at position 28 by G, substituting E at position 41 by M, substituting C at position 145 by S, and substituting T at position 158 by I in the amino acid sequence of KGr). The transverse axis indicates wavelength, and the vertical axis indicates fluorescence intensity. The term "em" indicates a fluorescence spectrum, and the term "ex" indicates an excitation spectrum.

Figure 4 shows the absorption spectrum of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting Y at position 64 by L in the amino acid sequence of KGr).

Figure 5 shows the absorption spectrum of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting Y at position 64 by M in the amino acid sequence of KGr).

Figure 6 shows the absorption spectrum of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting E at position 41 by L and substituting F at position 80 by G in the amino acid sequence of KGr).

Figure 7 shows the fluorescence and excitation spectrums of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting Y at position 64 by F in the amino acid sequence of KGr).

Figure 8 shows the absorption spectrum of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting Y at position 64 by F in the amino acid sequence of KGr).

Figure 9 shows the fluorescence and excitation spectrums of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting Y at position 64 by H in the amino acid sequence of KGr).

Figure 10 shows the absorption spectrum of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting Y at position 64 by H in the amino acid sequence of KGr).

Figure 11 shows the fluorescence and excitation spectrums of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting C at position 26 by V, substituting C at position 143 by S, and substituting P at position 199 by L in the amino acid sequence of KGr).

Figure 12 shows the absorption spectrum of a mutant of the chromoprotein (KGr) derived from *Cnidopus japonicus* of the present invention (a mutant obtained by substituting C at position 26 by V, substituting C at position 143 by S, and substituting P at position 199 by L in the amino acid sequence of KGr).

BEST MODE FOR CARRYING OUT THE INVENTION

[0021] The embodiments of the present invention will be described in detail below.

(1) Chromoprotein of the present invention

[0022] The chromoprotein of the present invention is characterized in that it is derived from *Cnidopus japonicus*, and has the following properties:

- (1) the absorption maximum wavelength is 610 nm, and fluorescence is not emitted;
- (2) the molar absorption coefficient is 66,700 at 610 nm; and
- (3) the pH sensitivity of light-absorbing property is stable at between pH 4 and pH 10.

[0023] *Cnidopus japonicus* is one type of sea anemone belonging to Anthozoa of Cnidaria. Among the types of sea anemone that can be seen in Japan, *Cnidopus japonicus* has the highest degree of color mutation. Its withers height is always low, and it has a large number of warts on the body wall thereof. It has approximately 200 short tentacles. A parent sea anemone discharges developed embryos from its oral part. The discharged embryos become attached to the body wall of the parent sea anemone. Thereafter, the embryos are further developed, and as a result, they become baby sea anemone. Thus, this sea anemone was named *Komochi Isoginchaku* (a Japanese name meaning "seed sea anemone"). This type of sea anemone is distributed in the intertidal zones on the rock coasts between Hokkaido and Boso Peninsula and also in the zones immediately below the intertidal zones.

[0024] It is to be noted that a chromoprotein having the aforementioned properties was isolated using *Cnidopus japonicus* as a starting material in the examples described later, but that the chromoprotein of the present invention may also be obtained from forms of sea anemone other than *Cnidopus japonicus* in some cases. Such a chromoprotein is also included in the scope of the present invention.

[0025] As described in the examples below, the chromoprotein of the present invention has an absorption maximum wavelength of 610 nm and does not emit fluorescence. In addition, the present chromoprotein has a molar absorption coefficient of 66,700 at 610 nm. The molar absorption coefficient represents the amount of absorbed photons per mole

of molecule. Since the chromoprotein of the present invention does not emit fluorescence, the chromoprotein of the present invention can be used: (1) as an acceptor molecule (energy receptor) in FRET; (2) in development of a system for converting the energy of applied light into energy other than the light; and (3) in introduction of a mutation into the amino acid sequence of the protein to modify it so that it emits fluorescence.

[0026] In addition, the chromoprotein of the present invention is characterized in that the pH sensitivity of light-absorbing properties is stable at between pH 4 and pH 10. That is to say, in the case of the chromoprotein of the present invention, the peak value of the absorption spectrum does not significantly fluctuate in the range between pH 4 and pH 10. Accordingly, even under the same conditions, the chromoprotein of the present invention can be used in a broad range of pH environments, and thus, the use of the chromoprotein *in vivo* has few restrictions.

[0027] The examples of the chromoprotein of the present invention include a chromoprotein having either one of the following amino acid sequences:

(a) the amino acid sequence shown in SEQ ID NO: 1; and

(b) an amino acid sequence comprising a deletion, substitution and/or addition of one or several amino acids with respect to the amino acid sequence shown in SEQ ID NO: 1, and having light-absorbing properties.

[0028] The scope of "one or several" in the phrase "an amino acid sequence comprising a deletion, substitution and/or addition of one or several amino acids" is not particularly limited in the present specification. For example, it means 1 to 20, preferably 1 to 10, more preferably 1 to 7, further preferably 1 to 5, and particularly preferably 1 to 3.

[0029] The term "light-absorbing properties" is used in the present specification to mean properties capable of absorbing light having a certain wavelength. For example, an absorption maximum wavelength may be 610 nm as in the case of the chromoprotein described in the present specification, or the value of the absorption maximum wavelength may also be shifted. It is preferable that the pH sensitivity of light-absorbing properties is stable at between pH 4 and pH 10.

[0030] The chromoprotein of the present invention having the amino acid sequence shown in SEQ ID NO: 1 in the sequence listing does not emit fluorescence. In the present invention, one or several amino acids are deleted, substituted, and/or added with respect to the amino acid sequence shown in SEQ ID NO: 1, so as to produce a protein having modified light-absorbing properties, or so as to produce a protein emitting fluorescence in some cases. The thus produced proteins are also included in the scope of the present invention.

[0031] A specific example of a fluorescent protein produced by such mutation of amino acids may be a fluorescent protein having an amino acid sequence, wherein, with respect to the amino acid sequence shown in SEQ ID NO: 1, alanine as an amino acid residue at position 28 is substituted by glycine, glutamic acid as an amino acid residue at position 41 is substituted by methionine, cysteine as an amino acid residue at position 145 is substituted by serine, and threonine as an amino acid residue at position 158 is substituted by isoleucine.

[0032] Other specific examples of a fluorescent protein produced by such mutation of amino acids may include: a chromoprotein having an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by leucine with respect to the amino acid sequence shown in SEQ ID NO: 1; a chromoprotein having an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by methionine with respect to the amino acid sequence shown in SEQ ID NO: 1; a chromoprotein having an amino acid sequence, wherein glutamic acid as an amino acid residue at position 41 is substituted by leucine, and phenylalanine as an amino acid residue at position 80 is substituted by glycine, with respect to the amino acid sequence shown in SEQ ID NO: 1; a chromoprotein capable of emitting fluorescence, which has an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by phenylalanine with respect to the amino acid sequence shown in SEQ ID NO: 1; a chromoprotein capable of emitting fluorescence, which has an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by histidine with respect to the amino acid sequence shown in SEQ ID NO: 1; and a chromoprotein capable of emitting fluorescence, which has an amino acid sequence, wherein cysteine as an amino acid residue at position 26 is substituted by valine, cysteine as an amino acid residue at position 143 is substituted by serine, and proline as an amino acid residue at position 199 is substituted by leucine, with respect to the amino acid sequence shown in SEQ ID NO: 1.

[0033] The method of obtaining the chromoprotein of the present invention is not particularly limited. The protein may be either a protein synthesized by chemosynthesis, or recombinant protein produced by a gene recombination technique.

[0034] Where a recombinant protein is produced, it is necessary to obtain DNA encoding the protein. Appropriate primers are designed by using information regarding the amino acid sequence shown in SEQ ID NO: 1 of the sequence listing of the present specification and the nucleotide sequence shown in SEQ ID NO: 2 thereof. Using these primers, PCR is carried out by using cDNA library derived from *Cnidopus japonicus* as a template, so that DNA encoding the chromoprotein of the present invention can be obtained. The chromoprotein of the present invention can be produced by introducing this DNA into an appropriate expression system. Expression in an expression system will be described

later in the present specification.

(2) DNA of the present invention

[0035] According to the present invention, a gene encoding the chromoprotein of the present invention is provided.

[0036] Specific examples of DNA encoding the chromoprotein of the present invention may include either one of the following DNAs:

(a) DNA encoding the amino acid sequence shown in SEQ ID NO: 1; and

(b) DNA encoding an amino acid sequence, which comprises a deletion, substitution and/or addition of one or several amino acids with respect to the amino acid sequence shown in SEQ ID NO: 1, and has light-absorbing properties.

[0037] Other examples of DNA encoding the chromoprotein of the present invention may include either one of the following DNAs:

(a) the nucleotide sequence shown in SEQ ID NO: 2; and

(b) a nucleotide sequence comprising a deletion, substitution and/or addition of one or several nucleotides with respect to the nucleotide sequence shown in SEQ ID NO: 2, and encoding a protein having light-absorbing properties.

[0038] Further, examples of the DNA having the nucleotide sequence comprising a deletion, substitution and/or addition of one or several nucleotides with respect to the nucleotide sequence shown in SEQ ID NO: 2, and encoding a protein having light-absorbing properties, may include DNA having the nucleotide sequence shown in any one of SEQ ID NOS: 12, 14, 16, 18, 20, or 22.

[0039] The DNA of the present invention can be synthesized by, for example, the phosphoramidite method, or it can also be produced by polymerase chain reaction (PCR) using specific primers. The DNA of the present invention is produced by the method described above in the specification.

[0040] A method of introducing a desired mutation into a certain nucleic acid sequence is known to a person skilled in the art. For example, known techniques such as a site-directed mutagenesis, PCR using degenerated oligonucleotides, or the exposure of cells containing nucleic acid to mutagens or radioactive rays, are appropriately used, so as to construct DNA having a mutation. Such known techniques are described in, for example, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY., 1989; and Current Protocols in Molecular Biology, Supplements 1 to 38, John Wiley & Sons (1987-1997).

(3) Recombinant vector of the present invention

[0041] The DNA of the present invention can be inserted into a suitable vector and used. The type of a vector used in the present invention is not particularly limited. For example, it may be either a vector that can autonomously replicate (e.g., a plasmid, etc.), or vector that is incorporated into the genomes of host cells when it is introduced into the host cells and is then replicated together with the chromosome into which it is incorporated.

[0042] The vector used in the present invention is preferably an expression vector. In an expression vector, elements necessary for transcription (e.g., a promoter, etc.) are functionally ligated to the DNA of the present invention. The promoter is a DNA sequence which shows a transcriptional activity in host cells, and it is appropriately selected depending on the type of host cells.

[0043] Examples of a promoter which can operate in bacterial cells may include a *Bacillus stearothermophilus* maltogenic amylase gene promoter, a *Bacillus licheniformis* alpha-amylase gene promoter, a *Bacillus amyloliquefaciens* BAN amylase gene promoter, a *Bacillus subtilis* alkaline protease gene promoter, a *Bacillus pumilus* xylosidase gene promoter, P_H and P_L promoters of phage rhamda, and lac, trp and tac promoters of

Escherichia coli.

[0044] Examples of a promoter which can operate in mammalian cells may include an SV40 promoter, an MT-1 (metallothionein gene) promoter, and an adenovirus-2 major late promoter. Examples of a promoter which can operate in insect cells may include a polyhedrin promoter, a P10 promoter, an *Autographa californica* polyhedrosis basic protein promoter, a baculovirus immediate-early gene 1 promoter, and a baculovirus 39K delayed-early gene promoter. Examples of a promoter which can operate in yeast host cells may include promoters derived from yeast glycolytic genes, an alcohol dehydrogenase gene promoter, a TPI1 promoter, and an ADH2-4c promoter.

[0045] Examples of a promoter which can operate in filamentous cells may include an ADH3 promoter and a *tpiA* promoter.

[0046] In addition, an appropriate terminator such as a human growth hormone terminator, or a TPI1 terminator or ADH3 terminator for fungal cells, may be functionally bound to the DNA of the present invention, as necessary. The recombinant vector of the present invention may further have elements such as a polyadenylation signal (e.g., one derived from SV40 or the adenovirus 5E1b region), a transcription enhancer sequence (e.g., an SV40 enhancer), or a translation enhancer sequence (e.g., one encoding the adenovirus VA RNA).

[0047] The recombinant vector of the present invention may further comprise a DNA sequence which enables the replication of the recombinant vector in host cells. SV40 replication origin is an example of such a sequence (when the host cells are mammalian cells).

[0048] The recombinant vector of the present invention may further comprise a selective marker. Examples of such a selective marker may include genes, complements of which are absent from host cells, such as a dihydrofolate reductase (DHFR) gene or a *Shizosaccharomyces pombe* TPI gene, and drug resistant genes such as ampicillin, kanamycin, tetracycline, chloramphenicol, neomycin or hygromycin-resistant genes.

[0049] A method for ligating the DNA of the present invention, a promoter and, as desired, a terminator and/or a secretory signal sequence to one another and inserting these items into a suitable vector is known to a person skilled in the art.

(4) Transformant of the present invention

[0050] A transformant can be produced by introducing the DNA or recombinant vector of the present invention into a suitable host.

[0051] Any cell can be used as a host cell into which the DNA or recombinant vector of the present invention is introduced, as long as the DNA construct of the present invention can be expressed therein. Examples of such a cell may include bacteria, yeasts, fungal cells, and higher eukaryotic cells.

[0052] Examples of bacteria may include Gram-positive bacteria such as *Bacillus* or *Streptomyces*, and Gram-negative bacteria such as *Escherichia coli*. These bacteria may be transformed by the protoplast method or other known methods, using competent cells.

[0053] Examples of mammalian cells may include HEK 293 cells, HeLa cells, COS cells, BHK cells, CHL cells, and CHO cells. A method of transforming mammalian cells and expressing the introduced DNA sequence in the cells is also known. Examples of such a method may include the electroporation, the calcium phosphate method, and the lipofection method.

[0054] Examples of yeast cells may include those belonging to *Saccharomyces* or *Shizosaccharomyces*. Examples of such cells may include *Saccharomyces cerevisiae* and *Saccharomyces kluyveri*. Examples of a method of introducing a recombinant vector into yeast host cells may include the electroporation, the spheroplast method, and the lithium acetate method.

[0055] Examples of other fungal cells may include those belonging to *Filamentous fungi* such as *Aspergillus*, *Neurospora*, *Fusarium* or *Trichoderma*. Where *Filamentous fungi* are used as host cells, transformation can be carried out by incorporating DNA constructs into host chromosomes, so as to obtain recombinant host cells. Incorporation of DNA constructs into the host chromosomes is carried out by known methods, and such known methods may include homologous recombination and heterologous recombination.

[0056] Where insect cells are used as host cells, both a vector into which a recombinant gene is introduced and a baculovirus are co-introduced into insect cells, and a recombinant virus is obtained in the culture supernatant of the insect cells. Thereafter, insect cells are infected with the recombinant virus, so as to allow the cells to express proteins (described in, for example, *Baculovirus Expression Vectors, A Laboratory Manual*; and *Current Protocols in Molecular Biology, Bio/Technology*, 6, 47 (1988)).

[0057] The *Autographa californica* nuclear polyhedrosis virus, which is a virus infecting to insects belonging to *Barathra brassicae*, can be used as baculovirus.

[0058] Examples of insect cells used herein may include Sf9 and Sf21, which are *Spodoptera frugiperda* ovarian cells [*Baculovirus Expression Vectors, A Laboratory Manual*, W. H. Freeman & Company, New York, (1992)], and HiFive (manufactured by Invitrogen), which are *Trichoplusia ni* ovarian cells.

[0059] Examples of the method of co-introducing both a vector into which a recombinant gene has been introduced and the above baculovirus into insect cells to prepare a recombinant virus may include the calcium phosphate method and the lipofection method.

[0060] The above transformant is cultured in an appropriate nutritive medium under conditions enabling the introduced DNA construct to be expressed. In order to isolate and purify the protein of the present invention from the culture product of the transformant, common methods of isolating and purifying proteins may be used.

[0061] For example, where the protein of the present invention is expressed in a state dissolved in cells, after com-

pletion of the culture, cells are recovered by centrifugal separation, and the recovered cells are suspended in a water type buffer. Thereafter, the cells are disintegrated using an ultrasonic disintegrator or the like, so as to obtain a cell-free extract. A supernatant is obtained by centrifuging the cell-free extract, and then, a purified sample can be obtained from the supernatant by applying, singly or in combination, the following ordinary protein isolation and purification methods: the solvent extraction, the salting-out method using ammonium sulfate or the like, the desalting method, the precipitation method using an organic solvent, the anion exchange chromatography using resins such as diethylaminoethyl (DEAE) sepharose, the cation exchange chromatography using resins such as S-Sepharose FF (manufactured by Pharmacia), the hydrophobic chromatography using resins such as butyl sepharose or phenyl sepharose, the gel filtration method using a molecular sieve, the affinity chromatography, the chromatofocusing method, and the electrophoresis such as isoelectric focusing.

(5) Use of the chromoprotein of the present invention and a fusion protein comprising the same

[0062] The chromoprotein of the present invention can be fused with another protein, so as to construct a fusion protein. The type of said another protein to be fused to the chromoprotein of the present invention is not particularly limited, and preferred examples may include a protein which interacts with another molecule. The examples may include a receptor protein or ligand thereof, antigen, antibody and the like.

[0063] A method of obtaining the fusion protein of the present invention is not particularly limited. It may be either a protein synthesized by chemosynthesis, or recombinant protein produced by a gene recombination technique.

[0064] Where a recombinant fusion protein is produced, it is necessary to obtain DNA encoding the protein. The DNA encoding the chromoprotein of the present invention and the DNA encoding the another protein to be fused to the chromoprotein, can be obtained by the method as mentioned above in this specification or by the method similar to it. Then, these DNA fragments are ligated to one another by a gene recombination technique, so that DNA encoding the desired fusion protein can be obtained. This DNA is then introduced into an appropriate expression system, so that the fusion protein of the present invention can be produced.

[0065] FRET (fluorescence resonance energy transfer) has been known as a means for analyzing the interaction between molecules. In FRET, for example, a first molecule labeled with a cyan fluorescent protein (CFP) acting as a first fluorescent protein is allowed to coexist with a second molecule labeled with a yellow fluorescent protein (YFP) acting as a second fluorescent protein, so as to allow the yellow fluorescent protein (YFP) to act as an acceptor molecule and to allow the cyan fluorescent protein (CFP) to act as a donor molecule. Thus, FRET (fluorescence resonance energy transfer) is allowed to take place between both molecules, so as to visualize the interaction between the first and second molecules. Namely, in FRET, different dyes are introduced into two types of molecules. One dyes with a higher energy level (a donor molecule) is selectively excited, and the fluorescence of the dye is measured. Long-wavelength fluorescence from the other dye (an acceptor molecule) is also measured. The interaction between the molecules is visualized by using the difference between the amounts of both fluorescences. Only when both dyes are adjacent to each other due to the interaction of the two types of molecules, a decrease in the fluorescence of the donor molecule and an increase in the fluorescence of the acceptor molecule are observed by single wavelength excitation dual wavelength photometry. However, in a case where a chromoprotein is used as an acceptor molecule, a decrease in the fluorescence of the donor molecule occurs only when both dyes are adjacent to each other by the interaction of the two types of molecules. Such a decrease can be observed by single wavelength excitation single wavelength photometry. Thus, the use of the chromoprotein of the present invention enables facilitation of measurement apparatuses.

[0066] The chromoprotein of the present invention is particularly advantageous when it is used as an acceptor molecule in FRET (fluorescence resonance energy transfer). That is to say, a fused form (a first fused form) of the chromoprotein of the present invention and a test substance is first produced. Then, a fused form (a second fused form) of another test substance interacting with the above test substance and another fluorescent protein is produced. Thereafter, the first fused form is allowed to interact with the second fused form, and the generated fluorescence is analyzed, so that the interaction between the aforementioned two types of test substances can be analyzed. FRET (fluorescence resonance energy transfer) using the chromoprotein of the present invention may be carried out either in a test tube or in a cell.

(6) Kit of the present invention

[0067] The present invention provides a light-absorbing reagent kit comprising at least one which is selected from the chromoprotein, fusion protein, DNA, recombinant vector or transformant, which are described in the present specification. The kit of the present invention can be produced from commonly used materials that are known per se, by using common methods.

[0068] Reagents such as the chromoprotein or the DNA are dissolved in an appropriate solvent, so that the reagents

can be prepared in a form suitable for conservation. Water, ethanol, various types of buffer solution, etc. can be used as such a solvent.

[0069] The present invention will be further described in the following examples. However, the present invention is not limited by these examples.

EXAMPLES

Example 1: Isolation of gene encoding novel chromoprotein from sea anemone

(1) Extraction of total RNA

[0070] A chromoprotein gene was isolated from sea anemone emitting a green color. *Cnidopus japonicus* emitting a green color was used as a material. Frozen *Cnidopus japonicus* was crushed in a mortar. 7.5 ml of "TRIzol" (GIBCO BRL) was added to 1 g (wet weight) of *Cnidopus japonicus*, and the mixture was homogenized, followed by centrifugation at $1,500 \times g$ for 10 minutes. 1.5 ml of chloroform was added to the supernatant. The mixture was stirred for 15 seconds and then left at rest for 3 minutes. The resultant product was centrifuged at $7,500 \times g$ for 15 minutes. 3.75 ml of isopropanol was added to the supernatant. The mixture was stirred for 15 seconds and then left at rest for 10 minutes. The resultant product was centrifuged at $17,000 \times g$ for 10 minutes. The supernatant was discarded, and 6 ml of 70% ethanol was added thereto. The obtained mixture was centrifuged at $17,000 \times g$ for 10 minutes. The supernatant was discarded, and the precipitate was dissolved in 200 μ l of DEPC water. Total RNA dissolved in the DEPC water was 100 times diluted, and the values of O.D.260 and O.D.280 were measured, so as to determine the concentration of RNA. 1.2 mg of the total RNA was obtained from a green individual.

(2) Synthesis of first strand cDNA

[0071] cDNA (33 μ l) was synthesized from 4 μ g of the total RNA using a kit for synthesizing first strand cDNA, "Ready To Go" (Amersham Pharmacia).

(3) Degenerated PCR

[0072] Using 3 μ l out of the synthesized first strand cDNA (33 μ l) as a template, PCR was carried out. Primers were designed and produced by comparing the amino acid sequences of known fluorescent proteins, extracting similar portions, and converting them into nucleotide sequences. The sequences of the used primers are shown below:

5'-GGIGSICCIHTISCITT-3' (primer 1) (SEQ ID NO: 3);

and

5'-AACTGGAAGAATTCGCGGCCGCAGAATTTTTTTTTTTTTTTT-3' (primer 2)

(SEQ ID NO: 4),

wherein I represents inosine, S represents C or G, and H represents A, T, or C.

Composition of PCR reaction solution	
Template (first strand cDNA)	3 μ l
X 10 taq buffer	5 μ l
2.5 mM dNTPs	4 μ l
100 uM primer 3	1 μ l
100 uM primer 4	1 μ l
Milli Q	35 μ l
Taq polymerase (5 U/ μ l)	1 μ l

PCR reaction conditions

94°C, 1 minute (PAD)

94°C, 30 seconds (denaturation)

52°C, 30 seconds (annealing of the primers to the template)

72°C, 1 minute (elongation of the primers)

[0073] 30 cycles consisting of the above 3 steps were carried out. The annealing temperature was decreased 0.3°C per cycle. That is to say, the annealing temperature in the 30th cycle was 43°C.

72°C, 7 minutes (final elongation)

Retention at 4°C

[0074] Using 1 µl of an amplified product obtained as a result of the first PCR reaction as a template, PCR was carried out once again under the same conditions. A 800-bp fragment (derived from the green individual) was cut out by agarose gel electrophoresis and then purified. This 800-bp fragment contained a 3'-UTR portion as a whole.

(4) Subcloning and sequencing

[0075] The purified DNA fragment was ligated to a pT7-blue vector (Novagen). *Escherichia coli* (TG1) was transformed with the vector, and the obtained transformants were subjected to blue white selection. Thereafter, plasmid DNA was purified from white colonies of *Escherichia coli*. The nucleotide sequence of the inserted DNA fragment was determined by a DNA sequencer. The obtained nucleotide sequence was compared with the nucleotide sequences of other fluorescent protein genes to confirm that the nucleotide sequence of the DNA was derived from a fluorescent protein. 5'-RACE and 3'-RACE methods were applied to a gene that had been confirmed to be a part of a fluorescent protein gene, so as to carry out the cloning of a full-length gene.

(5) 5'-RACE method

[0076] In order to determine the nucleotide sequence of the 5'-terminal side of the DNA fragment obtained by de-generated PCR, the 5'-RACE method was applied using 5'-RACE System for Rapid Amplification of cDNA Ends, Version 2.0 (GIBCO BRL). 3 µg of the total RNA prepared in (1) above was used as a template.

[0077] For the first amplification of DC-tailed cDNA of the green individual, the following primers were used:

5'-GGCCACGCGTCGACTAGTACGGGIIIGGGIIIGGGIIG-3' (primer 3) (SEQ ID NO:

5);

and

5'-AGACGAGGCAATTTCCATCAAG-3' (primer 4) (SEQ ID NO: 6),

wherein I represents inosine.

[0078] For the second amplification, the following primers were used:

5'-GGCCACGCGTCGACTAGTAC-3' (primer 5) (SEQ ID NO: 7);

and

5'-GGCTACGCTTCCATATTGGCAGTT-3' (primer 6) (SEQ ID NO: 8).

PCR reaction conditions and the like were determined in accordance with the protocols attached with the kit.

[0079] The 350-bp amplified band was cut out by agarose gel electrophoresis and then purified. The purified DNA fragment was ligated to a pT7-blue vector (Novagen). *Escherichia coli* (TG1) was transformed with the vector, and the obtained transformants were subjected to blue white selection. Thereafter, plasmid DNA was purified from white colonies of *Escherichia coli*. The nucleotide sequence of the inserted DNA fragment was determined by a DNA sequencer. The entire nucleotide sequence is shown in SEQ ID NO: 2, and the entire amino acid sequence is shown in SEQ ID

NO: 1.

Example 2: Expression of protein in *Escherichia coli*

[0080] Primers corresponding to the N- and C-termini of the protein were produced from the obtained full-length nucleotide sequence. PCR was carried out using the primers and the first strand cDNA prepared in (2) above as a template. The used primers are as follows:

5'-CGGGATCCGACCATGGCTTCCAAAATCAGC-3' (primer 7) (SEQ ID NO: 9);

and

5'-CCGGAATTCTTAATTGTGACCAAGTTTAGATGGGCA-3' (primer 8) (SEQ ID NO: 10).

Composition of PCR reaction solution	
Template (first strand cDNA)	3 μ l
X 10 pyrobest buffer	5 μ l
2.5 mM dNTPs	4 μ l
100 μ M primer 7	1 μ l
100 μ M primer 8	1 μ l
Milli Q	35 μ l
Pyrobest polymerase (5 U/ μ l)	1 μ l

PCR reaction conditions

94°C, 1 minute (PAD)

94°C, 30 seconds (denaturation)

55°C, 30 seconds (annealing of the primers to the template)

72°C, 1 minute (elongation of the primers)

[0081] 30 cycles consisting of the above 3 steps were carried out.

72°C, 7 minutes (final elongation)

Retention at 4°C

[0082] An amplified band of approximately 700 bp was cut out by agarose gel electrophoresis and then purified. The purified DNA fragment was subcloned into the *Bam*HI-*Eco*RI site of a pRSET vector (Invitrogen), and it was then allowed to express in *Escherichia coli* (JM109-DE3). Since the expressed protein was constructed such that His-tag was attached to the N-terminus thereof, it was purified with Ni-Agarose gel (QIAGEN). Purification was carried out in accordance with the attached protocols.

Example 3: Analysis of protein

(1) Analysis of light-absorbing properties

[0083] The light-absorbing properties of the protein expressed in Example 2 were analyzed.

[0084] An absorption spectrum was measured using a 50 mM HEPES solution (pH 7.5) containing a 20 μ M chromo-protein. A molar absorption coefficient was calculated from the peak value of this spectrum. In the case of the chromo-protein derived from the green individual (referred to as KGr), the absorption peak was observed at 610 nm, and no fluorescence was detected (Table 1, Figure 1).

Table 1

Properties of chromoprotein (KGr)					
Absorption maximum	Fluorescence maximum	Molar absorption coefficient	quantum yield	pH sensitivity	Number of amino acids
610 nm	-	66,700 (610 nm)	-	Non	232

(1) Measurement of pH sensitivity

The pH sensitivity of the protein expressed in Example 2 was analyzed.

The absorption spectrum of the protein was measured in the following 100 mM buffer solution (Figure 2).

The following buffer solutions were used for each pH:

pH 4 and 5: Acetate buffer

pH 6: MES buffer

pH 7 and 8: HEPES buffer

pH 9 and 10: Glycine buffer

The peak value did not significantly change at any pH.

Example 4: Modification of KGr

[0085] In KGr, A at position 28 was substituted by G, E at position 41 was substituted by M, C at position 145 was substituted by S, and T at position 158 was substituted by I, so that the KGr was modified to have an absorption peak at 444 nm and to emit yellow fluorescence with a peak at 534 nm (Figure 3).

Example 5: Modification of properties of KGr by amino acid substitution

[0086] Y at position 64 that is a chromophore-forming amino acid (QYG) of KGr was substituted by L or M, so that the absorption peak became 418 nm and so that the absorption peak was shifted from the original absorption peak at 610 nm to the shorter wavelength side (Figures 1 and 2). The amino acid sequence of the protein wherein Y at position 64 was substituted by L is shown in SEQ ID NO: 11, and the nucleotide sequence thereof is shown in SEQ ID NO: 12. The amino acid sequence of the protein wherein Y at position 64 was substituted by M is shown in SEQ ID NO: 13, and the nucleotide sequence thereof is shown in SEQ ID NO: 14.

[0087] E at position 41 was substituted by L, and F at position 80 was substituted by G, so that the absorption peak became 528 nm and so that the absorption peak was shifted from the original absorption peak at 610 nm to the shorter wavelength side (Figure 3). The amino acid sequence of this protein is shown in SEQ ID NO: 15, and the nucleotide sequence thereof is shown in SEQ ID NO: 16.

[0088] Y at position 64 that is a chromophore-forming amino acid (QYG) was substituted by F, so that the absorption peak became 412 nm, and so that the absorption peak was shifted from the original absorption peak at 610 nm to the shorter wavelength side and the protein was further modified to emit fluorescence with a peak at 504 nm (Figures 4 and 5). The amino acid sequence of this protein is shown in SEQ ID NO: 17, and the nucleotide sequence thereof is shown in SEQ ID NO: 18.

[0089] Y at position 64 that is a chromophore-forming amino acid (QYG) was substituted by H, so that the absorption peak became 418 nm, and so that the absorption peak was shifted from the original absorption peak at 610 nm to the shorter wavelength side and the protein was further modified to emit fluorescence with a peak at 520 nm (Figures 6 and 7). The amino acid sequence of this protein is shown in SEQ ID NO: 19, and the nucleotide sequence thereof is shown in SEQ ID NO: 20.

[0090] C at position 26 was substituted by V, C at position 143 was substituted by S, and P at position 199 was substituted by L, so that the absorption peak became 585 nm, and so that the absorption peak was shifted from the original absorption peak at 610 nm to the shorter wavelength side and the protein was further modified to emit fluorescence with a peak at 625 nm. This fluorescent protein was defined as KGr Rb (Figures 8 and 9). The amino acid sequence of this protein is shown in SEQ ID NO: 21, and the nucleotide sequence thereof is shown in SEQ ID NO: 22.

INDUSTRIAL APPLICABILITY

[0091] The present invention provides a novel chromoprotein derived from *Cnidopus japonicus*. The chromoprotein

of the present invention has desired fluorescence properties and low pH sensitivity. Thus, it is useful for molecular biology analysis.

5

10

15

20

25

30

35

40

45

50

55

SEQUENCE LISTING

<110> RIKEN

<120> Chromo protein

<130> A31347A

<160> 22

<210> 1

<211> 232

<212> PRT

<213> Cnidopus japonicus

<400> 1

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

1 5 10 15

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

20 25 30

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

35 40 45

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Tyr

50 55 60

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

85 90 95

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

100 105 110

Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro

115 120 125

EP 1 512 744 A1

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys
 130 135 140
 5
 Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met
 145 150 155 160
 10
 Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
 165 170 175
 15
 Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe
 180 185 190
 His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly
 20
 195 200 205
 Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr
 25
 210 215 220
 Cys Pro Ser Lys Leu Gly His Asn
 225 230
 30
 <210> 2
 35
 <211> 699
 <212> DNA
 <213> Cnidopus japonicus
 40
 <400> 2
 atg gct tcc aaa atc agc gac aat gta cgt atc aag tta tat atg gag 48
 45
 Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu
 1 5 10 15
 ggc aca gtc aac aat cat cac ttc atg tgc gaa gct gaa gga gag ggc 96
 50
 Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly
 20 25 30
 55
 aag cca tac gag gga act caa atg gag aac ata aaa gtc acc aaa gga 144

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly
 5 35 40 45
 ggc cct ctg ccg ttc tct ttt gat atc ttg acg cct aac tgc caa tat 192
 Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Tyr
 10 50 55 60
 gga agc gta gcc ata acc aag tat aca tca ggg att cca gac tac ttt 240
 Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe
 15 65 70 75 80
 aag caa tct ttt cct gaa gga ttt acc tgg gaa aga acc aca atc tac 288
 20 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr
 85 90 95
 25 gaa gat ggg gct tac ctt aca act caa caa gaa acc aaa ctt gat gga 336
 Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly
 100 105 110
 30 aat tgc ctc gtc tac aat att aaa atc ctt gga tgt aat ttt ccc ccc 384
 Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro
 35 115 120 125
 aat ggt cct gtg atg cag aag aaa acc caa ggc tgg gaa ccc tgt tgc 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys
 40 130 135 140
 gag atg cgc tat aca cgt gat ggt gtg cta tgt ggc caa aca tta atg 480
 45 Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met
 145 150 155 160
 50 gca ctt aaa tgc gcc gat ggg aac cac ctc act tgc cat ctg aga act 528
 Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
 165 170 175
 55 act tac agg tcc aaa aag gca gca aag gcg ttg cag atg cca ccc ttc 576

Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe
 180 185 190
 cat ttt tca gac cat cgt cct gaa ata gtg aag gtt tca gag aac ggc 624
 His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly
 195 200 205
 aca cta ttt gaa cag cac gaa agt tca gtg gcc agg tac tgt caa aca 672
 Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr
 210 215 220
 tgc cca tct aaa ctt ggt cac aat taa 699
 Cys Pro Ser Lys Leu Gly His Asn
 225 230
 <210> 3
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic DNA
 <400> 3
 ggigsiccih tiscitt 17
 <210> 4
 <211> 44
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic DNA

<400> 4

aactggaaga attcgcggcc gcagaatttt tttttttttt tttt 44

<210> 5

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 5

ggccacgcgt cgactagtag gggiigggii gggiig 36

<210> 6

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 6

agacgaggca atttccatca ag 22

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 7

ggccacggt cgactagtag

20

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 8

ggctacgctt ccatattggc agtt

24

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 9

cgggatccga ccatggcttc caaaatcagc

30

<210> 10

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 10

ccggaattct taattgtgac caagtttaga tgggca 36

<210> 11

<211> 232

<212> PRT

<213> Cnidopus japonicus

<400> 11

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

1 5 10 15

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

20 25 30

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

35 40 45

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Leu

50 55 60

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

85 90 95

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

100 105 110

Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro

115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys

130 135 144

Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met

145 150 155 160
 5 Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
 165 170 175
 10 Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe
 180 185 190
 15 His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly
 195 200 205
 20 Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr
 210 215 220
 25 Cys Pro Ser Lys Leu Gly His Asn
 225 230
 30 <210> 12
 <211> 699
 <212> DNA
 <213> Cnidopus japonicus
 35 <400> 12
 atg gct tcc aaa atc agc gac aat gta cgt atc aag tta tat atg gag 48
 Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu
 40 1 5 10 15
 ggc aca gtc aac aat cat cac ttc atg tgc gaa gct gaa gga gag ggc 96
 45 Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly
 20 25 30
 50 aag cca tac gag gga act caa atg gag aac ata aaa gtc acc aaa gga 144
 Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly
 35 40 45
 55 ggc cct ctg ccg ttc tct ttt gat atc ttg acg cct aac tgc caa ctt 192

EP 1 512 744 A1

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Leu
50 55 60
5 gga agc gta gcc ata acc aag tat aca tca ggg att cca gac tac ttt 240
Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe
10 65 70 75 80
aag caa tct ttt cct gaa gga ttt acc tgg gaa aga acc aca atc tac 288
15 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr
85 90 95
gaa gat ggg gct tac ctt aca act caa caa gaa acc aza ctt gat gga 336
20 Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly
100 105 110
25 aat tgc ctc gtc tac aat att aaa atc ctt gga tgt aat ttt ccc ccc 384
Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro
115 120 125
30 aat ggt cct gtg atg cag aag aaa acc caa ggc tgg gaa ccc tgt tgc 432
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys
130 135 144
35 gag atg cgc tat aca cgt gat ggt gtg cta tgt ggc caa aca tta atg 480
Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met
40 145 150 155 160
gca ctt aaa tgc gcc gat ggg aac cac ctc act tgc cat ctg aga act 528
45 Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
165 170 175
50 act tac agg tcc aaa aag gca gca aag gcg ttg cag atg cca ccc ttc 576
Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe
180 185 190
55 cat ttt tca gac cat cgt cct gaa ata gtg aag gtt tca gag aac ggc 624

His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly

195

200

205

aca cta ttt gaa cag cac gaa agt tca gtg gcc agg tac tgt caa aca 672

Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr

210

215

220

tgc cca tct aaa ctt ggt cac aat taa

699

Cys Pro Ser Lys Leu Gly His Asn

225

230

<210> 13

<211> 232

<212> PRT

<213> Chidopus japonicus

<400> 13

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

1

5

10

15

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

20

25

30

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

35

40

45

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Met

50

55

60

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65

70

75

80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

85

90

95

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

100 105 110
 Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro
 5 115 120 125
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys
 10 130 135 140
 Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met
 15 145 150 155 160
 Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
 165 170 175
 20 Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe
 180 185 190
 25 His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly
 195 200 205
 Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr
 30 210 215 220
 Cys Pro Ser Lys Leu Gly His Asn
 35 225 230
 40 <210> 14
 <211> 699
 <212> DNA
 45 <213> Cnidopus japonicus
 <400> 14
 50 atg gct tcc aaa atc agc gac aat gta cgt atc aag tta tat atg gag 48
 Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu
 1 5 10 15
 55 ggc aca gtc aac aat cat cac ttc atg tgc gaa gct gaa gga gag ggc 96

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

5

20

25

30

aag cca tac gag gga act caa atg gag aac ata aaa gtc acc aaa gga 144

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

10

35

40

45

ggc cct ctg ccg ttc tct ttt gat atc ttg acg cct aac tgc caa atg 192

15

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Met

50

55

60

gga agc gta gcc ata acc aag tat aca tca ggg att cca gac tac ttt 240

20

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65

70

75

80

25

aag caa tct ttt cct gaa gga ttt acc tgg gaa aga acc aca atc tac 288

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

30

85

90

95

gaa gat ggg gct tac ctt aca act caa caa gaa acc aaa ctt gat gga 336

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

35

100

105

110

aat tgc ctc gtc tac aat att aaa atc ctt gga tgt aat ttt ccc ccc 384

40

Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro

115

120

125

aat ggt cct gtg atg cag aag aaa acc caa ggc tgg gaa ccc tgt tgc 432

45

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys

130

135

140

50

gag atg cgc tat aca cgt gat ggt gtg cta tgt ggc caa aca tta atg 480

Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met

145

150

155

160

55

gca ctt aaa tgc gcc gat ggg aac cac ctc act tgc cat ctg aga act 528

Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr

165 170 175

act tac agg tcc aaa aag gca gca aag gcg ttg cag atg cca ccc ttc 576

Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe

180 185 190

cat ttt tca gac cat cgt cct gaa ata gtg aag gtt tca gag aac ggc 624

His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly

195 200 205

aca cta ttt gaa cag cac gaa agt tca gtg gcc agg tac tgt caa aca 672

Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr

210 215 220

tgc cca tct aaa ctt ggt cac aat taa 699

Cys Pro Ser Lys Leu Gly His Asn

225 230

<210> 15

<211> 232

<212> PRT

<213> Cnidopus japonicus

<400> 15

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

1 5 10 15

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

20 25 30

Lys Pro Tyr Glu Gly Thr Gln Met Leu Asn Ile Lys Val Thr Lys Gly

35 40 45

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Met

EP 1 512 744 A1

	50	55	60
5	Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Gly		
	65	70	75 80
	Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr		
10		85	90 95
	Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly		
15		100	105 110
	Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro		
	115	120	125
20	Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys		
	130	135	140
25	Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met		
	145	150	155 160
	Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr		
30		165	170 175
	Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe		
35		180	185 190
	His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly		
	195	200	205
40	Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr		
	210	215	220
45	Cys Pro Ser Lys Leu Gly His Asn		
	225	230	
50			
	<210> 16		
	<211> 699		
55	<212> DNA		

<213> Cnidopus japonicus

<400> 16

5

atg gct tcc aaa atc agc gac aat gta cgt atc aag tta tat atg ctg 48

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

10

1

5

10

15

ggc aca gtc aac aat cat cac ttc atg tgc gaa gct gaa gga gag ggc 96

15

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

20

25

30

aag cca tac gag gga act caa atg ctt aac ata aaa gtc acc aaa gga 144

20

Lys Pro Tyr Glu Gly Thr Gln Met Leu Asn Ile Lys Val Thr Lys Gly

35

40

45

25

ggc cct ctg ccg ttc tct ttt gat atc ttg acg cct aac tgc caa tat 192

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Met

50

55

60

30

gga agc gta gcc ata acc aag tat aca tca ggg att cca gac tac ggt 240

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Gly

35

65

70

75

80

aag caa tct ttt cct gaa gga ttt acc tgg gaa aga acc aca atc tac 288

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

40

85

90

95

gaa gat ggg gct tac ctt aca act caa caa gaa acc aaa ctt gat gga 336

45

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

100

105

110

50

aat tgc ctc gtc tac aat att aaa atc ctt gga tgt aat ttt ccc ccc 384

Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro

115

120

125

55

aat ggt cct gtg atg cag aag aaa acc caa ggc tgg gaa ccc tgt tgc 432

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys

130

135

140

gag atg cgc tat aca cgt gat ggt gtg cta tgt ggc caa aca tta atg 480

Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met

145

150

155

160

gca ctt aaa tgc gcc gat ggg aac cac ctc act tgc cat ctg aga act 528

Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr

165

170

175

act tac agg tcc aaa aag gca gca aag gcg ttg cag atg cca ccc ttc 576

Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe

180

185

190

cat ttt tca gac cat cgt cct gaa ata gtg aag gtt tca gag aac ggc 624

His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly

195

200

205

aca cta ttt gaa cag cac gaa agt tca gtg gcc agg tac tgt caa aca 672

Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr

210

215

220

tgc cca tct aaa ctt ggt cac aat taa

699

Cys Pro Ser Lys Leu Gly His Asn

225

230

<210> 17

<211> 232

<212> PRT

<213> Cnidopus japonicus

<400> 17

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

	5	10	15
5	Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly		
	20	25	30
10	Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly		
	35	40	45
	Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Phe		
15	50	55	60
	Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe		
	65	70	75
20	Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr		
	85	90	95
25	Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly		
	100	105	110
30	Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro		
	115	120	125
	Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys		
35	130	135	140
	Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met		
40	145	150	155
	Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr		
	165	170	175
45	Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe		
	180	185	190
50	His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly		
	195	200	205
	Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr		
55	210	215	220

Cys Pro Ser Lys Leu Gly His Asn

225

230

<210> 18

<211> 699

<212> DNA

<213> Cnidopus japonicus

<400> 18

atg gct tcc aaa atc agc gac aat gta cgt atc aag tta tat atg gag 48

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

5

10

15

ggc aca gtc aac aat cat cac ttc atg tgc gaa gct gaa gga gag ggc 96

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

20

25

30

aag cca tac gag gga act caa atg gag aac ata aaa gtc acc aaa gga 144

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

35

40

45

ggc cct ctg ccg ttc tct ttt gat atc ttg acg cct aac tgc caa ttt 192

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Phe

50

55

60

gga agc gta gcc ata acc aag tat aca tca ggg att cca gac tac ttt 240

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65

70

75

80

aag caa tct ttt cct gaa gga ttt acc tgg gaa aga acc aca atc tac 288

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

85

90

95

gaa gat ggg gct tac ctt aca act caa caa gaa acc aaa ctt gat gga 336

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly
 5 100 105 110
 aat tgc ctc gtc tac aat att aaa atc ctt gga tgt aat ttt ccc ccc 384
 Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro
 10 115 120 125
 aat ggt cct gtg atg cag aag aaa acc caa ggc tgg gaa ccc tgt tgc 432
 15 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys
 130 135 140
 gag atg cgc tat aca cgt gat ggt gtg cta tgt ggc caa aca tta atg 480
 20 Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met
 145 150 155 160
 25 gca ctt aaa tgc gcc gat ggg aac cac ctc act tgc cat ctg aga act 528
 Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
 30 165 170 175
 act tac agg tcc aaa aag gca gca aag gcg ttg cag atg cca ccc ttc 576
 35 Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe
 180 185 190
 cat ttt tca gac cat cgt cct gaa ata gtg aag gtt tca gag aac ggc 624
 40 His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly
 195 200 205
 45 aca cta ttt gaa cag cac gaa agt tca gtg gcc agg tac tgt caa aca 672
 Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr
 210 215 220
 50 tgc cca tct aaa ctt ggt cac aat taa 699
 Cys Pro Ser Lys Leu Gly His Asn
 55 225 230

<210> 19

<211> 232

<212> PRT

<213> Cnidopus japonicus

<400> 19

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

1 5 10 15

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

20 25 30

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

35 40 45

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln His

50 55 60

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

85 90 95

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

100 105 110

Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro

115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys

130 135 140

Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met

145 150 155 160

Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr

165 170 175

Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe

180

185

190

His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly

195

200

205

Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr

210

215

220

Cys Pro Ser Lys Leu Gly His Asn

225

230

<210> 20

<211> 699

<212> DNA

<213> Cnidopus japonicus

<400> 20

atg gct tcc aaa atc agc gac aat gta cgt atc aag tta tat atg gag 48

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

1

5

10

15

ggc aca gtc aac aat cat cac ttc atg tgc gaa gct gaa gga gag ggc 96

Gly Thr Val Asn Asn His His Phe Met Cys Glu Ala Glu Gly Glu Gly

20

25

30

aag cca tac gag gga act caa atg gag aac ata aaa gtc acc aaa gga 144

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

35

40

45

ggc cct ctg ccg ttc tct ttt gat atc ttg acg cct aac tgc caa cat 192

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln His

50

55

60

gga agc gta gcc ata acc aag tat aca tca ggg att cca gac tac ttt 240

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65 70 75 80

aag caa tct ttt cct gaa gga ttt acc tgg gaa aga acc aca atc tac 288

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

85 90 95

gaa gat ggg gct tac ctt aca act caa caa gaa acc aaa ctt gat gga 336

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

100 105 110

aat tgc ctc gtc tac aat att aaa atc ctt gga tgt aat ttt ccc ccc 384

Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro

115 120 125

aat ggt cct gtg atg cag aag aaa acc caa ggc tgg gaa ccc tgt tgc 432

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Cys Cys

130 135 140

gag atg cgc tat aca cgt gat ggt gtg cta tgt ggc caa aca tta atg 480

Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met

145 150 155 160

gca ctt aaa tgc gcc gat ggg aac cac ctc act tgc cat ctg aga act 528

Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr

165 170 175

act tac agg tcc aaa aag gca gca aag gcg ttg cag atg cca ccc ttc 576

Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe

180 185 190

cat ttt tca gac cat cgt cct gaa ata gtg aag gtt tca gag aac ggc 624

His Phe Ser Asp His Arg Pro Glu Ile Val Lys Val Ser Glu Asn Gly

195 200 205

aca cta ttt gaa cag cac gaa agt tca gtg gcc agg tac tgt caa aca 672

Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr

210 215 220

tgc cca tct aaa ctt ggt cac aat taa

699

Cys Pro Ser Lys Leu Gly His Asn

225 230

<210> 21

<211> 232

<212> PRT

<213> Cnidopus japonicus

<400> 21

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

1 5 10 15

Gly Thr Val Asn Asn His His Phe Met Val Glu Ala Glu Gly Glu Gly

20 25 30

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

35 40 45

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Met

50 55 60

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

85 90 95

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

100 105 110

Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro

115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Cys

130 135 140

Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met

145 150 155 160

Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr

165 170 175

Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe

180 185 190

His Phe Ser Asp His Arg Leu Glu Ile Val Lys Val Ser Glu Asn Gly

195 200 205

Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr

210 215 220

Cys Pro Ser Lys Leu Gly His Asn

225 230

<210> 22

<211> 699

<212> DNA

<213> *Cnidopus japonicus*

<400> 22

atg gct tcc aaa atc agc gac aat gta cgt atc aag tta tat atg gag 48

Met Ala Ser Lys Ile Ser Asp Asn Val Arg Ile Lys Leu Tyr Met Glu

1 5 10 15

ggc aca gtc aac aat cat cac ttc atg gtc gaa gct gaa gga gag ggc 96

Gly Thr Val Asn Asn His His Phe Met Val Glu Ala Glu Gly Glu Gly

20 25 30

aag cca tac gag gga act caa atg gag aac ata aaa gtc acc aaa gga 144

Lys Pro Tyr Glu Gly Thr Gln Met Glu Asn Ile Lys Val Thr Lys Gly

35

40

45

ggc cct ctg ccg ttc tct ttt gat atc ttg acg cct aac tgc caa tat 192

Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Asn Cys Gln Met

50

55

60

gga agc gta gcc ata acc aag tat aca tca ggg att cca gac tac ttt 240

Gly Ser Val Ala Ile Thr Lys Tyr Thr Ser Gly Ile Pro Asp Tyr Phe

65

70

75

80

aag caa tct ttt cct gaa gga ttt acc tgg gaa aga acc aca atc tac 288

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Ile Tyr

85

90

95

gaa gat ggg gct tac ctt aca act caa caa gaa acc aaa ctt gat gga 336

Glu Asp Gly Ala Tyr Leu Thr Thr Gln Gln Glu Thr Lys Leu Asp Gly

100

105

110

aat tgc ctc gtc tac aat att aaa atc ctt gga tgt aat ttt ccc ccc 384

Asn Cys Leu Val Tyr Asn Ile Lys Ile Leu Gly Cys Asn Phe Pro Pro

115

120

125

aat ggt cct gtg atg cag aag aaa acc caa ggc tgg gaa ccc agt tgc 432

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Cys

130

135

140

gag atg cgc tat aca cgt gat ggt gtg cta tgt ggc caa aca tta atg 480

Glu Met Arg Tyr Thr Arg Asp Gly Val Leu Cys Gly Gln Thr Leu Met

145

150

155

160

gca ctt aaa tgc gcc gat ggg aac cac ctc act tgc cat ctg aga act 528

Ala Leu Lys Cys Ala Asp Gly Asn His Leu Thr Cys His Leu Arg Thr

165

170

175

act tac agg tcc aaa aag gca gca aag gcg ttg cag atg cca ccc ttc 576

Thr Tyr Arg Ser Lys Lys Ala Ala Lys Ala Leu Gln Met Pro Pro Phe

180

185

190

cat ttt tca gac cat cgt ctt gaa ata gtg aag gtt tca gag aac ggc 624

His Phe Ser Asp His Arg Leu Glu Ile Val Lys Val Ser Glu Asn Gly

195

200

205

aca cta ttt gaa cag cac gaa agt tca gtg gcc agg tac tgt caa aca 672

Thr Leu Phe Glu Gln His Glu Ser Ser Val Ala Arg Tyr Cys Gln Thr

210

215

220

tgc cca tct aaa ctt ggt cac aat taa

699

Cys Pro Ser Lys Leu Gly His Asn

225

230

Claims

1. A chromoprotein derived from *Cnidopus japonicus* having the following properties:

- (1) the absorption maximum wavelength is 610 nm, and fluorescence is not emitted;
- (2) the molar absorption coefficient is 66,700 at 610 nm; and
- (3) the pH sensitivity of light-absorbing property is stable at between pH 4 and pH 10.

2. A chromoprotein having either one of the following amino acid sequences:

- (a) the amino acid sequence shown in SEQ ID NO: 1; and
- (b) an amino acid sequence comprising a deletion, substitution and/or addition of one or several amino acids with respect to the amino acid sequence shown in SEQ ID NO: 1, and having light-absorbing properties.

3. A chromoprotein capable of emitting fluorescence, which has an amino acid sequence, wherein, with respect to the amino acid sequence shown in SEQ ID NO: 1, alanine as an amino acid residue at position 28 is substituted by glycine, glutamic acid as an amino acid residue at position 41 is substituted by methionine, cysteine as an amino acid residue at position 145 is substituted by serine, and threonine as an amino acid residue at position 158 is substituted by isoleucine.

4. A chromoprotein having an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by leucine with respect to the amino acid sequence shown in SEQ ID NO: 1.

5. A chromoprotein having an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by methionine with respect to the amino acid sequence shown in SEQ ID NO: 1.

6. A chromoprotein having an amino acid sequence, wherein glutamic acid as an amino acid residue at position 41 is substituted by leucine, and phenylalanine as an amino acid residue at position 80 is substituted by glycine, with respect to the amino acid sequence shown in SEQ ID NO: 1.

7. A chromoprotein capable of emitting fluorescence, which has an amino acid sequence wherein tyrosine as an

amino acid residue at position 64 is substituted by phenylalanine with respect to the amino acid sequence shown in SEQ ID NO: 1.

- 5 8. A chromoprotein capable of emitting fluorescence, which has an amino acid sequence wherein tyrosine as an amino acid residue at position 64 is substituted by histidine with respect to the amino acid sequence shown in SEQ ID NO: 1.
9. A chromoprotein capable of emitting fluorescence, which has an amino acid sequence, wherein cysteine as an amino acid residue at position 26 is substituted by valine, cysteine as an amino acid residue at position 143 is substituted by serine, and proline as an amino acid residue at position 199 is substituted by leucine, with respect to the amino acid sequence shown in SEQ ID NO: 1.
10. A DNA encoding the protein of any of claims 1 to 9.
- 15 11. A DNA of either one of followings:
 - (a) DNA encoding the amino acid sequence shown in SEQ ID NO: 1; and
 - (b) DNA encoding an amino acid sequence, which comprises a deletion, substitution and/or addition of one or several amino acids with respect to the amino acid sequence shown in SEQ ID NO: 1, and has light-absorbing properties.
- 20 12. A DNA having either one of the following nucleotide sequences:
 - (a) the nucleotide sequence shown in SEQ ID NO: 2; and
 - (b) a nucleotide sequence comprising a deletion, substitution and/or addition of one or several nucleotides with respect to the nucleotide sequence shown in SEQ ID NO: 2, and encoding a protein having light-absorbing properties.
- 25 13. A DNA having the nucleotide sequence shown in any one of SEQ ID NOS: 12, 14, 16, 18, 20, or 22.
- 30 14. A recombinant vector having the DNA of any of claims 10 to 13.
15. A transformant having the DNA of any of claims 10 to 13 or the recombinant vector of claim 14.
- 35 16. A fusion protein composed of the chromoprotein of any of claims 1 to 9 and another protein.
17. A method for analyzing a physiologically active substance, which is characterized in that the FRET (fluorescence resonance energy transfer) method is applied using the chromoprotein of any of claims 1 to 9 as an acceptor protein.
- 40 18. A light-absorbing reagent kit comprising the chromoprotein of any of claims 1 to 9, the DNA of any of claims 10 to 13, the recombinant vector of claim 14, the transformant of claim 15, or the fusion protein of claim 16.

Fig. 1

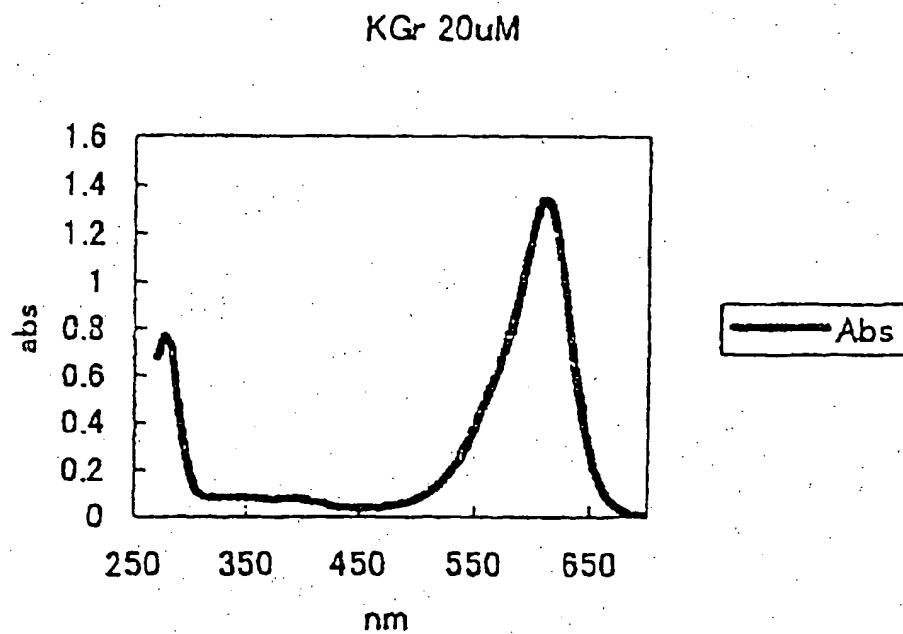


Fig. 2

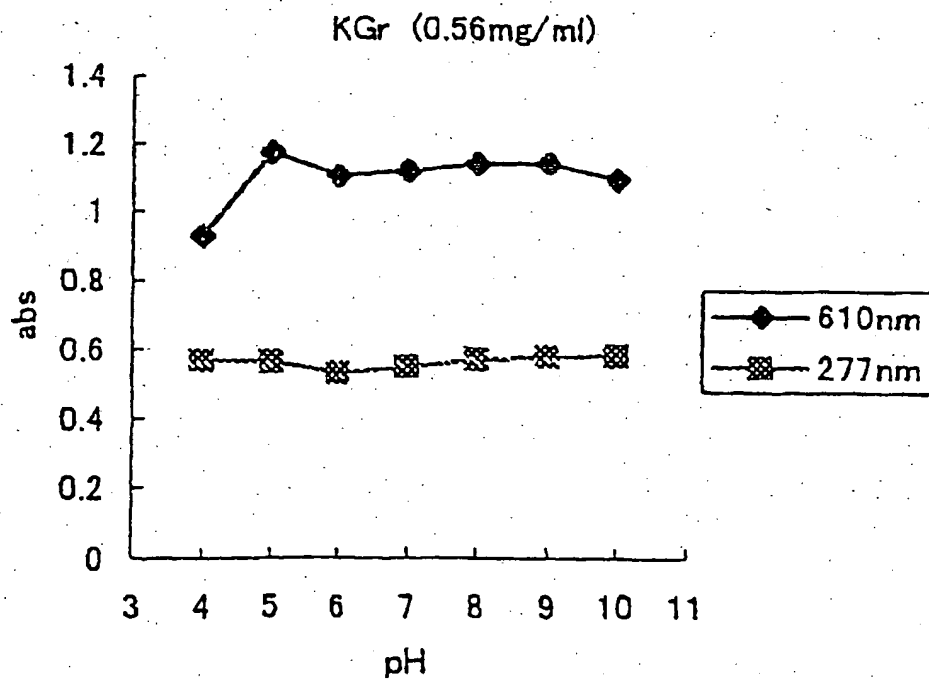


Fig. 3

KG A28G,E41M,C145S,T158I

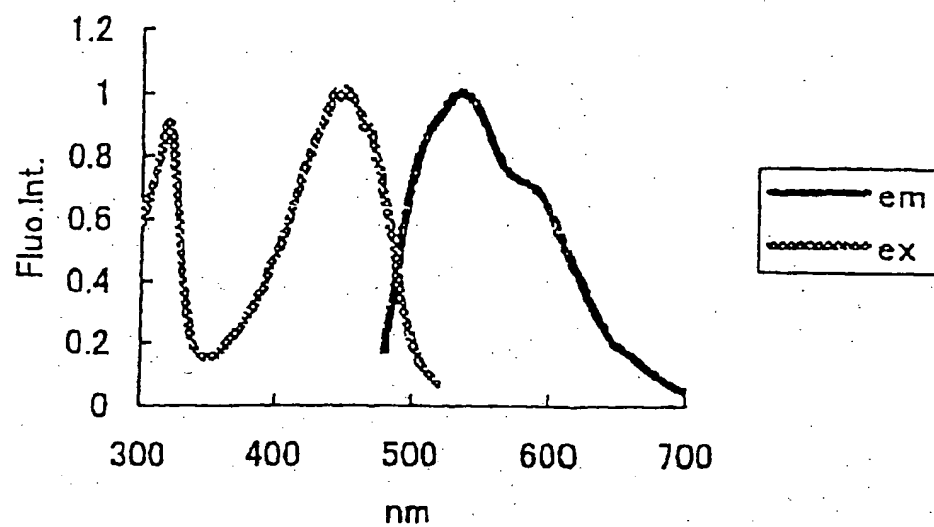


Fig. 4

Y64L

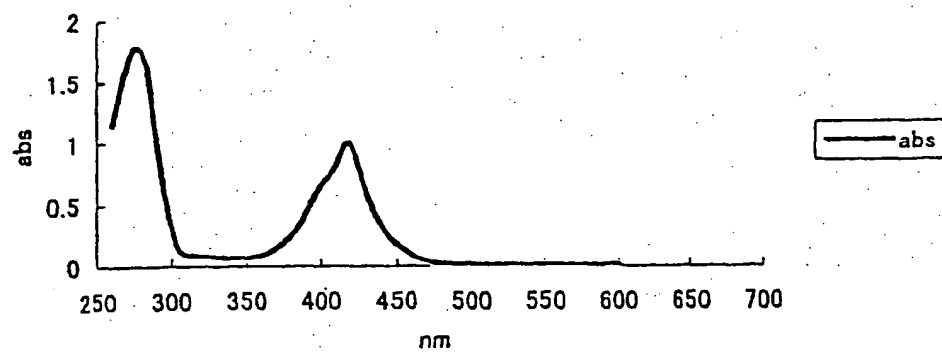


Fig. 5

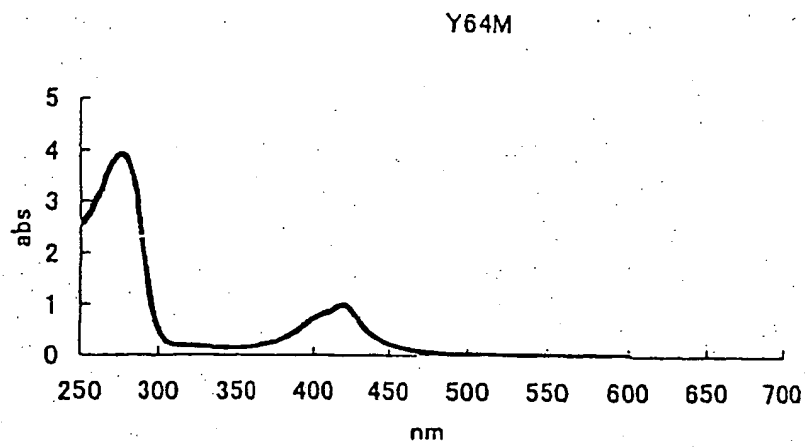


Fig. 6

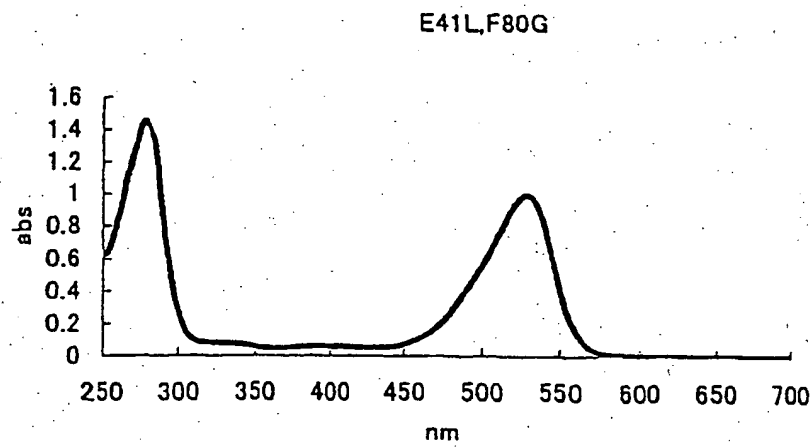


Fig. 7

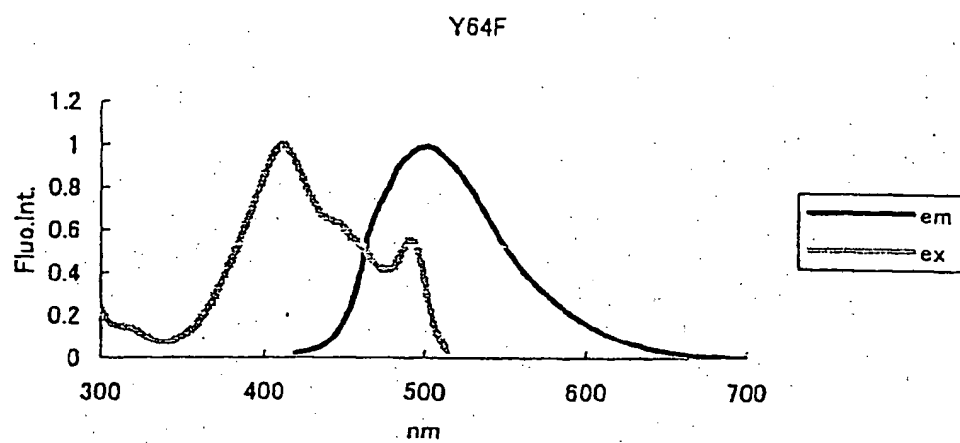


Fig. 8

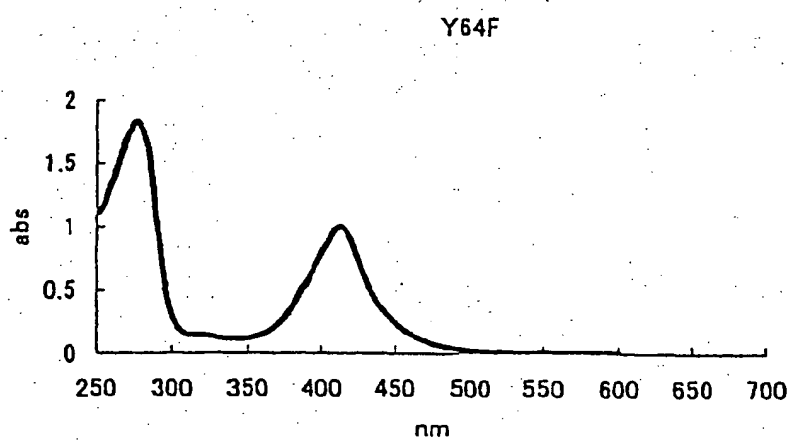


Fig. 9

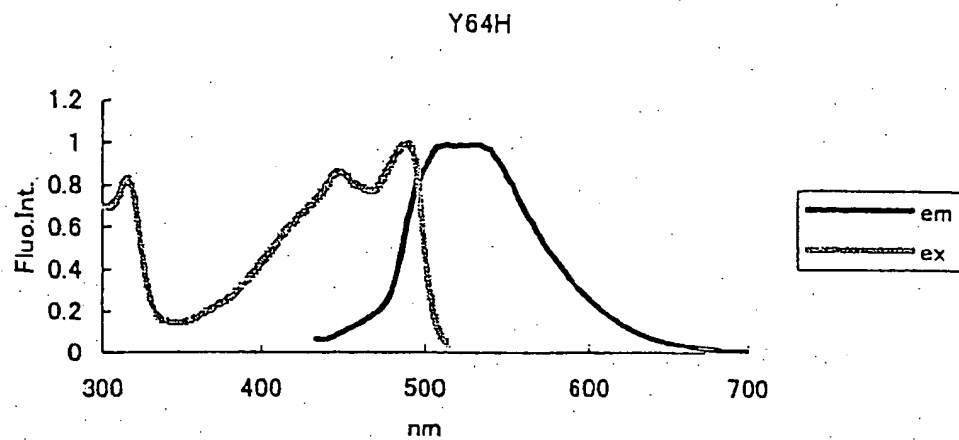


Fig. 10

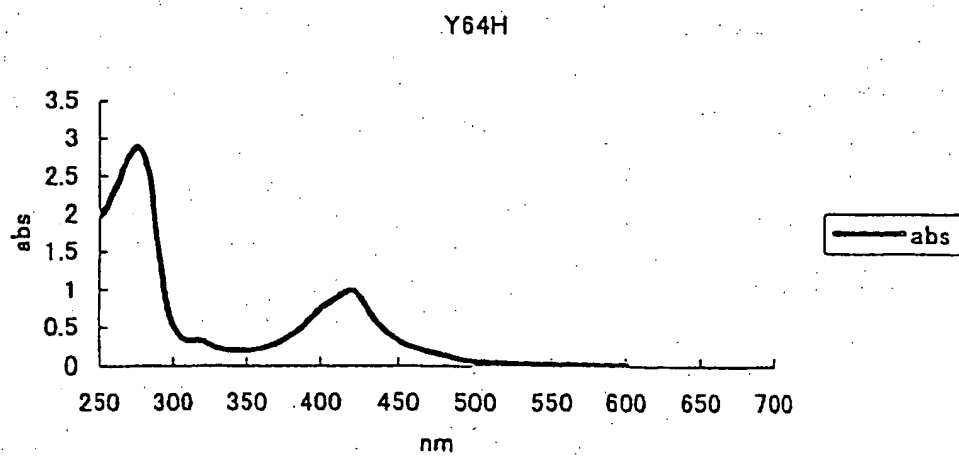


Fig. 11

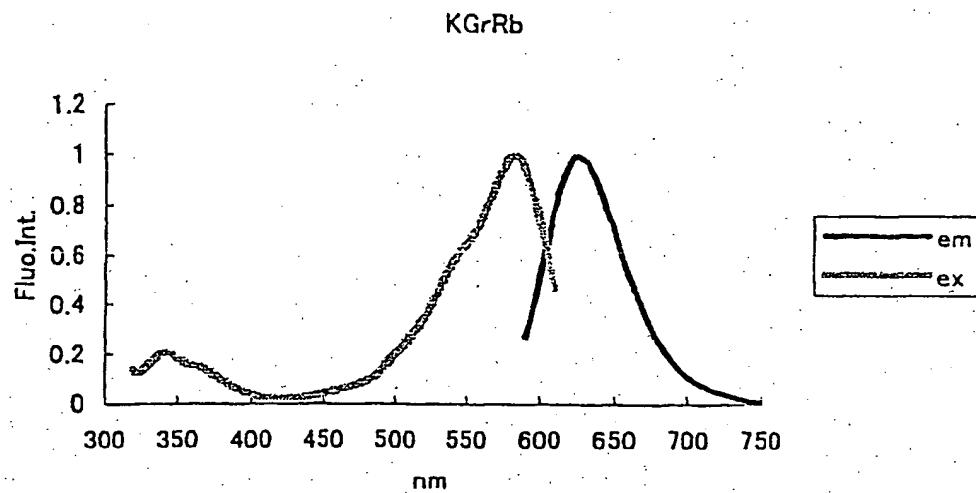
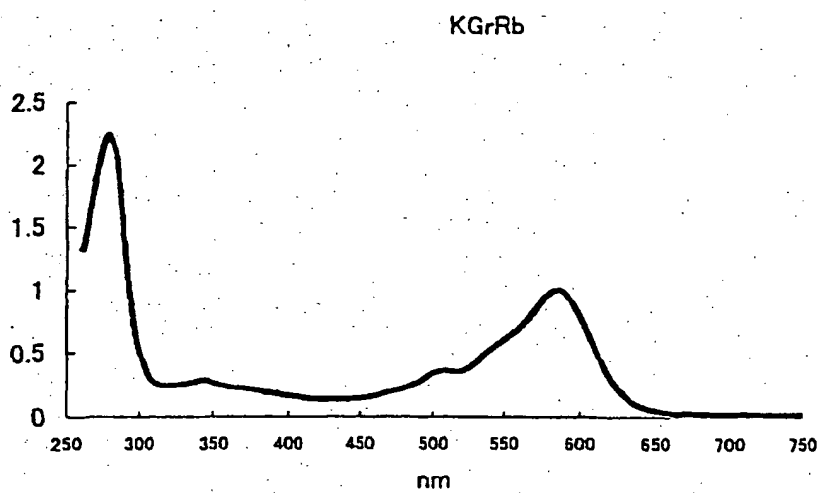


Fig. 12



INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/07336

A. CLASSIFICATION OF SUBJECT MATTER

Int.C1⁷ C12N15/12, 1/21, 5/10, C07K14/435, 19/00, G01N21/78

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int.C1⁷ C12N15/00-15/90, 1/21, 5/10, C07K14/00-14/825, 19/00,
G01N21/78

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE (STN), WPI/BIOSIS (DIALOG), JSTPlus (JOIS)
GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X.	Atsushi MIYAWAKI, "Shiho Dobutsu to Keiko Tanpaku-shitsu", Midoriishi, March, 2002, No.13, pages 1 to 4	1-18
A	WO 01/27150 A2 (CLONTECH LABORATORIES INC.), 19 April, 2001 (19.04.01), & EP 1305412 A2	1-18

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search
27 June, 2003 (27.06.03)Date of mailing of the international search report
15 July, 2003 (15.07.03)Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

Form PCT/ISA/210 (second sheet) (July 1998)